

SEQUENCE LISTING

<110> BASF Plant Science GmbH
SweTree Technologies AB

5

<120> IMPROVED CONSTRUCTS FOR MARKER EXCISION BASED ON DUAL-FUNCTION
SELECTION MARKER

10 <130> PF 55443 EP

<160> 16

<170> PatentIn version 3.1

15

<210> 1

<211> 1160

<212> DNA

<213> Rhodosporidium toruloides

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<220>

<221> CDS

<222> (1)..(1104)

<223> coding for DAAO

25

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Met	His	Ser	Gln	Lys	Arg	Val	Val	Val	Leu	Gly	Ser	Gly	Val	Ile	Gly	
1				5					10					15		

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ctg	agc	agc	gcc	ctc	atc	ctc	gct	cgg	aag	ggc	tac	agc	gtg	cat	att	96
Leu	Ser	Ser	Ala	Leu	Ile	Leu	Ala	Arg	Lys	Gly	Tyr	Ser	Val	His	Ile	
			20					25					30			

35

ctc	gcg	cgc	gac	ttg	ccg	gag	gac	gtc	tcg	agc	cag	act	ttc	gct	tca	144
Leu	Ala	Arg	Asp	Leu	Pro	Glu	Asp	Val	Ser	Ser	Gln	Thr	Phe	Ala	Ser	
		35					40					45				

40

cca	tgg	gct	ggc	gcg	aat	tgg	acg	cct	ttc	atg	acg	ctt	aca	gac	ggc	192
Pro	Trp	Ala	Gly	Ala	Asn	Trp	Thr	Pro	Phe	Met	Thr	Leu	Thr	Asp	Gly	
	50					55					60					

45

cct	cga	caa	gca	aaa	tgg	gaa	gaa	tcg	act	ttc	aag	aag	tgg	gtc	gag	240
Pro	Arg	Gln	Ala	Lys	Trp	Glu	Glu	Ser	Thr	Phe	Lys	Lys	Trp	Val	Glu	
65					70					75				80		

	ttg gtc ccg acg ggc cat gcc atg tgg ctc aag ggg acg agg cgg ttc	288
	Leu Val Pro Thr Gly His Ala Met Trp Leu Lys Gly Thr Arg Arg Phe	
	85 90 95	
5	gcg cag aac gaa gac ggc ttg ctc ggg cac tgg tac aag gac atc acg	336
	Ala Gln Asn Glu Asp Gly Leu Leu Gly His Trp Tyr Lys Asp Ile Thr	
	100 105 110	
10	cca aat tac cgc ccc ctc cca tct tcc gaa tgt cca cct ggc gct atc	384
	Pro Asn Tyr Arg Pro Leu Pro Ser Ser Glu Cys Pro Pro Gly Ala Ile	
	115 120 125	
15	ggc gta acc tac gac acc ctc tcc gtc cac gca cca aag tac tgc cag	432
	Gly Val Thr Tyr Asp Thr Leu Ser Val His Ala Pro Lys Tyr Cys Gln	
	130 135 140	
20	tac ctt gca aga gag ctg cag aag ctc ggc gcg acg ttt gag aga cgg	480
	Tyr Leu Ala Arg Glu Leu Gln Lys Leu Gly Ala Thr Phe Glu Arg Arg	
	145 150 155 160	
25	acc gtt acg tcg ctt gag cag gcg ttc gac ggt gcg gat ttg gtg gtc	528
	Thr Val Thr Ser Leu Glu Gln Ala Phe Asp Gly Ala Asp Leu Val Val	
	165 170 175	
30	aac gct acg gga ctt ggc gcc aag tcg att gcg ggc atc gac gac caa	576
	Asn Ala Thr Gly Leu Gly Ala Lys Ser Ile Ala Gly Ile Asp Asp Gln	
	180 185 190	
35	gcc gcc gag cca atc cgc ggg caa acc gtc ctc gtc aag tcc cca tgc	624
	Ala Ala Glu Pro Ile Arg Gly Gln Thr Val Leu Val Lys Ser Pro Cys	
	195 200 205	
40	aag cga tgc acg atg gac tcg tcc gac ccc gct tct ccc gcc tac atc	672
	Lys Arg Cys Thr Met Asp Ser Ser Asp Pro Ala Ser Pro Ala Tyr Ile	
	210 215 220	
45	att ccc cga cca ggt ggc gaa gtc atc tgc ggc ggg acg tac ggc gtg	720
	Ile Pro Arg Pro Gly Gly Glu Val Ile Cys Gly Gly Thr Tyr Gly Val	
	225 230 235 240	
50	gga gac tgg gac ttg tct gtc aac cca gag acg gtc cag cgg atc ctc	768
	Gly Asp Trp Asp Leu Ser Val Asn Pro Glu Thr Val Gln Arg Ile Leu	
	245 250 255	

3

aag cac tgc ttg cgc ctc gac ccg acc atc tcg agc gac gga acg atc 816
 Lys His Cys Leu Arg Leu Asp Pro Thr Ile Ser Ser Asp Gly Thr Ile
 260 265 270

5 gaa ggc atc gag gtc ctc cgc cac aac gtc ggc ttg cga cct gca cga 864
 Glu Gly Ile Glu Val Leu Arg His Asn Val Gly Leu Arg Pro Ala Arg
 275 280 285

10 cga ggc gga ccc cgc gtt gag gca gaa cgg atc gtc ctg cct ctc gac 912
 Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
 290 295 300

15 cgg aca aag tcg ccc ctc tcg ctc ggc agg ggc agc gca cga gcg gcg 960
 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
 305 310 315 320

20 aag gag aag gag gtc acg ctt gtg cat gcg tat ggc ttc tcg agt gcg 1008
 Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
 325 330 335

gga tac cag cag agt tgg ggc gcg gcg gag gat gtc gcg cag ctc gtc 1056
 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
 340 345 350

25 gac gag gcg ttc cag cgg tac cac ggc gcg gcg cgg gag tcg aag ttg 1104
 Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
 355 360 365

30 tagggcggga tttgtggctg tattgcgggc atctacaaga aaaaaaaaaa aaaaaa 1160

<210> 2
 <211> 368
 <212> PRT
 35 <213> Rhodosporidium toruloides

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40 Leu Ser Ser Ala Leu Ile Leu Ala Arg Lys Gly Tyr Ser Val His Ile
 20 25 30

45 Leu Ala Arg Asp Leu Pro Glu Asp Val Ser Ser Gln Thr Phe Ala Ser
 35 40 45

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10	Ala	Gln	Asn	Glu	Asp	Gly	Leu	Leu	Gly	His	Trp	Tyr	Lys	Asp	Ile	Thr	
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	Gly	Val	Thr	Tyr	Asp	Thr	Leu	Ser	Val	His	Ala	Pro	Lys	Tyr	Cys	Gln	
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20	Tyr	Leu	Ala	Arg	Glu	Leu	Gln	Lys	Leu	Gly	Ala	Thr	Phe	Glu	Arg	Arg	
	145					150					155					160	
	Thr	Val	Thr	Ser	Leu	Glu	Gln	Ala	Phe	Asp	Gly	Ala	Asp	Leu	Val	Val	
					165					170					175		
25	Asn	Ala	Thr	Gly	Leu	Gly	Ala	Lys	Ser	Ile	Ala	Gly	Ile	Asp	Asp	Gln	
				180					185					190			
	Ala	Ala	Glu	Pro	Ile	Arg	Gly	Gln	Thr	Val	Leu	Val	Lys	Ser	Pro	Cys	
30			195					200					205				
	Lys	Arg	Cys	Thr	Met	Asp	Ser	Ser	Asp	Pro	Ala	Ser	Pro	Ala	Tyr	Ile	
	210						215					220					
35	Ile	Pro	Arg	Pro	Gly	Gly	Glu	Val	Ile	Cys	Gly	Gly	Thr	Tyr	Gly	Val	
	225					230					235					240	
	Gly	Asp	Trp	Asp	Leu	Ser	Val	Asn	Pro	Glu	Thr	Val	Gln	Arg	Ile	Leu	
					245					250					255		
40	Lys	His	Cys	Leu	Arg	Leu	Asp	Pro	Thr	Ile	Ser	Ser	Asp	Gly	Thr	Ile	
				260					265					270			
	Glu	Gly	Ile	Glu	Val	Leu	Arg	His	Asn	Val	Gly	Leu	Arg	Pro	Ala	Arg	
45			275					280					285				

Arg Gly Gly Pro Arg Val Glu Ala Glu Arg Ile Val Leu Pro Leu Asp
 290 295 300

5 Arg Thr Lys Ser Pro Leu Ser Leu Gly Arg Gly Ser Ala Arg Ala Ala
 305 310 315 320

Lys Glu Lys Glu Val Thr Leu Val His Ala Tyr Gly Phe Ser Ser Ala
 325 330 335

10 Gly Tyr Gln Gln Ser Trp Gly Ala Ala Glu Asp Val Ala Gln Leu Val
 340 345 350

Asp Glu Ala Phe Gln Arg Tyr His Gly Ala Ala Arg Glu Ser Lys Leu
 15 355 360 365

<210> 3
 <211> 1005
 <212> DNA
 20 <213> *Caenorhabditis elegans*
 <220>
 <221> CDS
 <222> (1)..(1002)
 25 <223> coding for DAO

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gga tgt act tca gca ctt caa ata tca aaa gct ata cca aat gcg aaa 96
 Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
 20 25 30

35 ata act gtg ctc cac gat aaa cca ttt aaa aaa tcg tgc agt gca gga 144
 Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
 35 40 45

40 cca gca gga tta ttt aga atc gat tat gag gag aat act gaa tac gga 192
 Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
 50 55 60

cgt gct tct ttc gcc tgg ttc tca cat ctc tat cgc act aca aaa gga 240
 45 Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly

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5	tcc gaa acc ggc gtg aaa tta gtt tct gga cat att caa tcc gac aac Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn	288						
	85		90		95			
10	ttg gag tca ttg aag caa caa caa aga gcc tat ggc gat att gtg tac Leu Glu Ser Leu Lys Gln Gln Gln Arg Ala Tyr Gly Asp Ile Val Tyr	336						
	100		105		110			
15	aac ttt aga ttc ttg gat gat aga gaa cgg ctg gac att ttt ccc gaa Asn Phe Arg Phe Leu Asp Asp Arg Glu Arg Leu Asp Ile Phe Pro Glu	384						
	115		120		125			
20	cca tca aag cac tgc att cac tac acc gcc tac gca tca gaa ggt aac Pro Ser Lys His Cys Ile His Tyr Thr Ala Tyr Ala Ser Glu Gly Asn	432						
	130		135		140			
25	aag tac gtg cct tat ttg aag aat ttg ctg ctt gag caa aaa atc gag Lys Tyr Val Pro Tyr Leu Lys Asn Leu Leu Leu Glu Gln Lys Ile Glu	480						
	145		150		155		160	
30	ttc aag caa caa gaa gtg acg agt ttg gac gca gtc gcc gac gct ggt Phe Lys Gln Gln Glu Val Thr Ser Leu Asp Ala Val Ala Asp Ala Gly	528						
	165		170		175			
35	tac gat gtt att gta aac tgc gca ggc ttg tac ggt gga aag ttg gct Tyr Asp Val Ile Val Asn Cys Ala Gly Leu Tyr Gly Gly Lys Leu Ala	576						
	180		185		190			
40	ggt gat gac gat act tgc tac ccc att aga gga gtc att ttg gaa gtt Gly Asp Asp Asp Thr Cys Tyr Pro Ile Arg Gly Val Ile Leu Glu Val	624						
	195		200		205			
45	gat gca cca tgg cac aag cac ttc aat tat cga gac ttt act act ttc Asp Ala Pro Trp His Lys His Phe Asn Tyr Arg Asp Phe Thr Thr Phe	672						
	210		215		220			
50	aca att cca aaa gag cac agc gtg gtg gtt ggg tcc acc aag cag gac Thr Ile Pro Lys Glu His Ser Val Val Val Gly Ser Thr Lys Gln Asp	720						
	225		230		235		240	
55	aat cga tgg gat ttg gag atc acc gac gag gat aga aat gat att ttg Asn Arg Trp Asp Leu Glu Ile Thr Asp Glu Asp Arg Asn Asp Ile Leu	768						
	245		250		255			

aaa cga tac att gct tta cat cct gga atg aga gag cca aag att atc 816
 Lys Arg Tyr Ile Ala Leu His Pro Gly Met Arg Glu Pro Lys Ile Ile
 260 265 270

5

aaa gaa tgg tca gca ctt cgc ccg gga cgt aag cat gtc aga att gaa 864
 Lys Glu Trp Ser Ala Leu Arg Pro Gly Arg Lys His Val Arg Ile Glu
 275 280 285

10

gcg cag aag agg aca tct gtt gga aac tca aaa gat tat atg gtt gtg 912
 Ala Gln Lys Arg Thr Ser Val Gly Asn Ser Lys Asp Tyr Met Val Val
 290 295 300

15

cat cac tat ggt cac ggg agc aac gga ttc acg ttg ggt tgg gga aca 960
 His His Tyr Gly His Gly Ser Asn Gly Phe Thr Leu Gly Trp Gly Thr
 305 310 315 320

20

gca att gaa gca act aaa ctt gtt aag act gca cta gga tta taa 1005
 Ala Ile Glu Ala Thr Lys Leu Val Lys Thr Ala Leu Gly Leu
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<210> 4
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 <212> PRT
 25 <213> Caenorhabditis elegans

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 Met Ala Asn Ile Ile Pro Lys Ile Ala Ile Ile Gly Glu Gly Val Ile
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Gly Cys Thr Ser Ala Leu Gln Ile Ser Lys Ala Ile Pro Asn Ala Lys
 20 25 30

35

Ile Thr Val Leu His Asp Lys Pro Phe Lys Lys Ser Cys Ser Ala Gly
 35 40 45

Pro Ala Gly Leu Phe Arg Ile Asp Tyr Glu Glu Asn Thr Glu Tyr Gly
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40

Arg Ala Ser Phe Ala Trp Phe Ser His Leu Tyr Arg Thr Thr Lys Gly
 65 70 75 80

Ser Glu Thr Gly Val Lys Leu Val Ser Gly His Ile Gln Ser Asp Asn
 85 90 95

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<210> 5
 <211> 1186
 <212> DNA
 <213> Nectria haematococca

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<220>
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 <222> (42)..(1124)
 <223> coding for DAAO

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 Val Val Val Gly Ala Gly Val Ile Gly Leu Thr Ser Ala Leu Leu Leu
 10 15 20

20

tcc aag aac aag ggc aac aag atc acc gtc gtg gcc aag cac atg ccc 152
 Ser Lys Asn Lys Gly Asn Lys Ile Thr Val Val Ala Lys His Met Pro
 25 30 35

25

ggc gac tat gac gtt gaa tac gcc tcg cct ttt gct ggt gcc aac cac 200
 Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe Ala Gly Ala Asn His
 40 45 50

30

tcc ccc atg gcg acg gaa gag agc agc gaa tgg gaa cgt cgc act tgg 248
 Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp Glu Arg Arg Thr Trp
 55 60 65

35

tac gag ttt aag aga ctg gtc gag gag gtc cct gag gcc ggt gtt cat 296
 Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro Glu Ala Gly Val His
 70 75 80 85

ttc cag aag tct cgc atc cag agg cgc aat gtg gac act gaa aag gcg 344
 Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val Asp Thr Glu Lys Ala
 90 95 100

40

cag agg tct ggt ttc cca gac gcc ctc ttc tcg aaa gaa ccc tgg ttc 392
 Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser Lys Glu Pro Trp Phe
 105 110 115

45

aag aac atg ttt gag gac ttc cgt gag cag cac cct agc gag gtc atc 440
 Lys Asn Met Phe Glu Asp Phe Arg Glu Gln His Pro Ser Glu Val Ile

	120	125	130	
	ccc ggt tac gac tct ggc tgc gag ttc aca tcg gtg tgc atc aac acg			488
	Pro Gly Tyr Asp Ser Gly Cys Glu Phe Thr Ser Val Cys Ile Asn Thr			
5	135	140	145	
	gcc atc tac ctc ccc tgg ctc ctc ggc cag tgc atc aag aat ggc gtc			536
	Ala Ile Tyr Leu Pro Trp Leu Leu Gly Gln Cys Ile Lys Asn Gly Val			
10	150	155	160	165
	atc gtc aag cgc gcc atc ctc aac gac att agc gag gcc aag aag ctg			584
	Ile Val Lys Arg Ala Ile Leu Asn Asp Ile Ser Glu Ala Lys Lys Leu			
	170	175	180	
15	agc cac gcg ggc aag acg ccc aat atc atc gtc aac gcc acg ggt ctc			632
	Ser His Ala Gly Lys Thr Pro Asn Ile Ile Val Asn Ala Thr Gly Leu			
	185	190	195	
	ggc tcc tac aag ctg ggc ggt gtc gag gac aag acc atg gcg cct gcg			680
20	Gly Ser Tyr Lys Leu Gly Gly Val Glu Asp Lys Thr Met Ala Pro Ala			
	200	205	210	
	cgg gga cag att gtg gtt gtg cgc aac gag agc agc ccc atg ctc ctc			728
	Arg Gly Gln Ile Val Val Val Arg Asn Glu Ser Ser Pro Met Leu Leu			
25	215	220	225	
	act tca ggt gtc gag gac ggc ggt gct gat gtc atg tac ttg atg cag			776
	Thr Ser Gly Val Glu Asp Gly Gly Ala Asp Val Met Tyr Leu Met Gln			
30	230	235	240	245
	cga gca gct ggc ggt ggc acc atc ctg ggc ggt acc tac gac gtt ggc			824
	Arg Ala Ala Gly Gly Gly Thr Ile Leu Gly Gly Thr Tyr Asp Val Gly			
	250	255	260	
35	aac tgg gag tct cag cca gac ccc aac atc gcg aat cgc atc atg cag			872
	Asn Trp Glu Ser Gln Pro Asp Pro Asn Ile Ala Asn Arg Ile Met Gln			
	265	270	275	
	cgc atc gtc gag gtg cgg ccc gag att gcc aac ggc aag ggc gtc aag			920
40	Arg Ile Val Glu Val Arg Pro Glu Ile Ala Asn Gly Lys Gly Val Lys			
	280	285	290	
	ggg ctg agc gtg atc cga cac gcc gtc ggc atg cgg ccg tgg cga aag			968
	Gly Leu Ser Val Ile Arg His Ala Val Gly Met Arg Pro Trp Arg Lys			
45	295	300	305	

gac gga gtc agg atc gag gag gag aag ctg gat gat gag act tgg atc 1016
 Asp Gly Val Arg Ile Glu Glu Glu Lys Leu Asp Asp Glu Thr Trp Ile
 310 315 320 325
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 gtg cac aac tac gga cac tct gga tgg ggt tac cag ggt tcg tat ggt 1064
 Val His Asn Tyr Gly His Ser Gly Trp Gly Tyr Gln Gly Ser Tyr Gly
 330 335 340
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 tgt gct gag aat gta gtc cag ttg gtt gac aag gtc ggc aag gcg gcc 1112
 Cys Ala Glu Asn Val Val Gln Leu Val Asp Lys Val Gly Lys Ala Ala
 345 350 355
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 aag tct aag ctg tagttgaaaa ggcctgaatg agtaatagta attggatatt 1164
 Lys Ser Lys Leu
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 <212> PRT
 <213> Nectria haematococca
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 Ala Lys His Met Pro Gly Asp Tyr Asp Val Glu Tyr Ala Ser Pro Phe
 35 40 45
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 Ala Gly Ala Asn His Ser Pro Met Ala Thr Glu Glu Ser Ser Glu Trp
 50 55 60
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 Glu Arg Arg Thr Trp Tyr Glu Phe Lys Arg Leu Val Glu Glu Val Pro
 65 70 75 80
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 Glu Ala Gly Val His Phe Gln Lys Ser Arg Ile Gln Arg Arg Asn Val
 85 90 95
 45
 Asp Thr Glu Lys Ala Gln Arg Ser Gly Phe Pro Asp Ala Leu Phe Ser
 100 105 110

[illegible]

13

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 340 345 350

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<210> 7

<211> 1071

<212> DNA

10 <213> *Trigonopsis variabilis*

<220>

<221> CDS

<222> (1) .. (1068)

15 <223>

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gct ctt caa ctt ctt cgt aaa gga cat gag gtt aca att gtg tcc gag 96
 Ala Leu Gln Leu Leu Arg Lys Gly His Glu Val Thr Ile Val Ser Glu
 20 25 30

25 ttt acg ccc ggt gat ctt agt atc gga tat acc tcg cct tgg gca ggt 144
 Phe Thr Pro Gly Asp Leu Ser Ile Gly Tyr Thr Ser Pro Trp Ala Gly
 35 40 45

30 gcc aac tgg ctc aca ttt tac gat gga ggc aag tta gcc gac tac gat 192
 Ala Asn Trp Leu Thr Phe Tyr Asp Gly Gly Lys Leu Ala Asp Tyr Asp
 50 55 60

35 gcc gtc tct tat cct atc ttg cga gag ctg gct cga agc agc ccc gag 240
 Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu
 65 70 75 80

40 gct gga att cga ctc atc agc caa cgc tcc cat gtt ctc aag cgt gat 288
 Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp
 85 90 95

45 ctt cct aaa ctg gaa gtt gcc atg tcg gcc atc tgt caa cgc aat ccc 336
 Leu Pro Lys Leu Glu Val Ala Met Ser Ala Ile Cys Gln Arg Asn Pro
 100 105 110

14

	tgg	ttc	aaa	aac	aca	gtc	gat	tct	ttc	gag	att	atc	gag	gac	agg	tcc	384
	Trp	Phe	Lys	Asn	Thr	Val	Asp	Ser	Phe	Glu	Ile	Ile	Glu	Asp	Arg	Ser	
			115					120							125		
5	agg	att	gtc	cac	gat	gat	gtg	gct	tat	cta	gtc	gaa	ttt	cgt	tcc	gtt	432
	Arg	Ile	Val	His	Asp	Asp	Val	Ala	Tyr	Leu	Val	Glu	Phe	Arg	Ser	Val	
			130					135						140			
10	tgt	atc	cac	acc	gga	gtc	tac	ttg	aac	tgg	ctg	atg	tcc	caa	tgc	tta	480
	Cys	Ile	His	Thr	Gly	Val	Tyr	Leu	Asn	Trp	Leu	Met	Ser	Gln	Cys	Leu	
			145					150					155			160	
15	tcg	ctc	ggc	gcc	acg	gtg	ggt	aaa	cgt	cga	gtg	aac	cat	atc	aag	gat	528
	Ser	Leu	Gly	Ala	Thr	Val	Val	Lys	Arg	Arg	Val	Asn	His	Ile	Lys	Asp	
					165					170						175	
20	gcc	aat	tta	cta	cac	tcc	tca	gga	tca	cgc	ccc	gac	gtg	att	gtc	aac	576
	Ala	Asn	Leu	Leu	His	Ser	Ser	Gly	Ser	Arg	Pro	Asp	Val	Ile	Val	Asn	
					180					185					190		
25	tgt	agt	ggc	ctc	ttt	gcc	cgg	ttc	ttg	gga	ggc	gtc	gag	gac	aag	aag	624
	Cys	Ser	Gly	Leu	Phe	Ala	Arg	Phe	Leu	Gly	Gly	Val	Glu	Asp	Lys	Lys	
					195					200				205			
30	atg	tac	cct	att	cga	gga	caa	gtc	gtc	ctt	ggt	cga	aac	tct	ctt	cct	672
	Met	Tyr	Pro	Ile	Arg	Gly	Gln	Val	Val	Leu	Val	Arg	Asn	Ser	Leu	Pro	
			210					215					220				
35	ttt	atg	gcc	tcc	ttt	tcc	agc	act	cct	gaa	aaa	gaa	aac	gaa	gac	gaa	720
	Phe	Met	Ala	Ser	Phe	Ser	Ser	Thr	Pro	Glu	Lys	Glu	Asn	Glu	Asp	Glu	
			225					230					235			240	
40	gct	cta	tat	atc	atg	acc	cga	ttc	gat	ggc	act	tct	atc	att	ggc	ggc	768
	Ala	Leu	Tyr	Ile	Met	Thr	Arg	Phe	Asp	Gly	Thr	Ser	Ile	Ile	Gly	Gly	
					245					250						255	
45	tgt	ttc	caa	ccc	aac	aac	tgg	tca	tcc	gaa	ccc	gat	cct	tct	ctc	acc	816
	Cys	Phe	Gln	Pro	Asn	Asn	Trp	Ser	Ser	Glu	Pro	Asp	Pro	Ser	Leu	Thr	
					260					265					270		
50	cat	cga	atc	ctg	tct	aga	gcc	ctc	gac	cga	ttc	ccg	gaa	ctg	acc	aaa	864
	His	Arg	Ile	Leu	Ser	Arg	Ala	Leu	Asp	Arg	Phe	Pro	Glu	Leu	Thr	Lys	
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	Asp Gly Pro Leu Asp Ile Val Arg Glu Cys Val Gly His Arg Pro Gly	
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	Arg Glu Gly Gly Pro Arg Val Glu Leu Glu Lys Ile Pro Gly Val Gly	
	305 310 315 320	
10	ttt gtt gtc cat aac tat ggt gcc gcc ggt gct ggt tac caa tcc tct	1008
	Phe Val Val His Asn Tyr Gly Ala Ala Gly Ala Gly Tyr Gln Ser Ser	
	325 330 335	
15	tac ggc atg gct gat gaa gct gtt tct tac gtc gaa aga gct ctt act	1056
	Tyr Gly Met Ala Asp Glu Ala Val Ser Tyr Val Glu Arg Ala Leu Thr	
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	Arg Pro Asn Leu	
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35	Phe Thr Pro Gly Asp Leu Ser Ile Gly Tyr Thr Ser Pro Trp Ala Gly	
	35 40 45	
	Ala Asn Trp Leu Thr Phe Tyr Asp Gly Gly Lys Leu Ala Asp Tyr Asp	
	50 55 60	
40	Ala Val Ser Tyr Pro Ile Leu Arg Glu Leu Ala Arg Ser Ser Pro Glu	
	65 70 75 80	
45	Ala Gly Ile Arg Leu Ile Ser Gln Arg Ser His Val Leu Lys Arg Asp	
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 Ile Gly Leu Thr Thr Ala Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro
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30 cgt att aag gtg att gcc aag tat acg cct gaa gat cgt tct gta gaa 147
 Arg Ile Lys Val Ile Ala Lys Tyr Thr Pro Glu Asp Arg Ser Val Glu
 30 35 40

tac act tcc cct tgg gct ggc gca aat ttc tgt agc att tct gct act 195
 Tyr Thr Ser Pro Trp Ala Gly Ala Asn Phe Cys Ser Ile Ser Ala Thr
 45 50 55

35 gat gac aat gct ttg cgc tgg gat aaa atc act tac cat cgt ttc gcc 243
 Asp Asp Asn Ala Leu Arg Trp Asp Lys Ile Thr Tyr His Arg Phe Ala
 60 65 70

40 tac ttg gcg aaa act cgt cct gaa gca gga atc cgt ttt gct gat ctt 291
 Tyr Leu Ala Lys Thr Arg Pro Glu Ala Gly Ile Arg Phe Ala Asp Leu
 75 80 85 90

45 cga gaa ttg tgg gag tac gag ccg aaa cac gac aaa atc aga tcc tgg 339
 Arg Glu Leu Trp Glu Tyr Glu Pro Lys His Asp Lys Ile Arg Ser Trp
 95 100 105

18

	aat acc tat gtc aga gat ttc aaa gtt atc cct gaa aaa gat ctt cca	387
	Asn Thr Tyr Val Arg Asp Phe Lys Val Ile Pro Glu Lys Asp Leu Pro	
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	Gly Glu Cys Ile Tyr Gly His Lys Ala Thr Thr Phe Leu Ile Asn Ala	
	125 130 135	
10	cct cat tac ttg aat tat atg tac aag ctg ctc att gaa gct ggc gtc	483
	Pro His Tyr Leu Asn Tyr Met Tyr Lys Leu Leu Ile Glu Ala Gly Val	
	140 145 150	
15	gaa ttt gaa aag aaa gaa ttg agt cac atc aaa gag act gtc gaa gaa	531
	Glu Phe Glu Lys Lys Glu Leu Ser His Ile Lys Glu Thr Val Glu Glu	
	155 160 165 170	
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	Thr Pro Glu Ala Ser Val Val Phe Asn Cys Thr Gly Leu Trp Ala Ser	
	175 180 185	
	aaa ttg ggt ggc gtt gaa gac ccg gac gtt tat ccg act cgt gga cat	627
	Lys Leu Gly Gly Val Glu Asp Pro Asp Val Tyr Pro Thr Arg Gly His	
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	Val Val Leu Val Lys Ala Pro His Val Thr Glu Thr Arg Ile Leu Asn	
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	Gly Lys Asn Ser Asp Thr Tyr Ile Ile Pro Arg Pro Leu Asn Gly Gly	
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35	gtc att tgc ggc ggt ttc atg caa cca gga aac tgg gat cgt gaa att	771
	Val Ile Cys Gly Gly Phe Met Gln Pro Gly Asn Trp Asp Arg Glu Ile	
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40	cac cct gaa gac act ttg gat atc ctt aag aga aca tcg gct ttg atg	819
	His Pro Glu Asp Thr Leu Asp Ile Leu Lys Arg Thr Ser Ala Leu Met	
	255 260 265	
	cca gaa ttg ttc cac ggc aag ggt ccg gag ggt gct gaa att att caa	867
	Pro Glu Leu Phe His Gly Lys Gly Pro Glu Gly Ala Glu Ile Ile Gln	
	270 275 280	

19

	gaa tgt gtc gga ttc cgt cct tct cga aag ggt ggt gcc cgc gta gag	915
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	Leu Asp Val Val Pro Gly Thr Ser Val Pro Leu Val His Asp Tyr Gly	
	300 305 310	
10	gct tct ggc aca gga tac caa gct ggt tat ggt atg gct ctt gac tct	1011
	Ala Ser Gly Thr Gly Tyr Gln Ala Gly Tyr Gly Met Ala Leu Asp Ser	
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	Trp Ile Leu Ser Asp Leu Gly Leu Ala Pro Arg Ile Lys Val Ile Ala	
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	35 40 45	
	Gly Ala Asn Phe Cys Ser Ile Ser Ala Thr Asp Asp Asn Ala Leu Arg	
	50 55 60	
35	Trp Asp Lys Ile Thr Tyr His Arg Phe Ala Tyr Leu Ala Lys Thr Arg	
	65 70 75 80	
	Pro Glu Ala Gly Ile Arg Phe Ala Asp Leu Arg Glu Leu Trp Glu Tyr	
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 Gly Val Ile Gly Leu Thr Thr Ala Val Val Leu Ala Glu Arg Gly Arg
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 Arg Val Arg Leu Trp Thr Arg Glu Pro Ala Glu Arg Thr Thr Ser Val
 25 30 35 40
 30 gta gcg ggc ggg ctg tgg tgg ccg tac cgg atc gag ccg gtc gcg ctg 198
 Val Ala Gly Gly Leu Trp Trp Pro Tyr Arg Ile Glu Pro Val Ala Leu
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 gcc cag gcc tgg gcg ctg cgt tcc ctg gac gtg tac gag gag ctg gcg 246
 Ala Gln Ala Trp Ala Leu Arg Ser Leu Asp Val Tyr Glu Glu Leu Ala
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 Ala Arg Pro Gly Gln Thr Gly Val Arg Met Leu Glu Gly Val Leu Gly
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 40 gag acc ggc ctg gac gag gtg gac ggg tgg gcc gcg gcc cgg ctg ccg 342
 Glu Thr Gly Leu Asp Glu Val Asp Gly Trp Ala Ala Ala Arg Leu Pro
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22

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	Ala	Arg	Leu	Pro	Leu	Ile	Asp	Met	Ser	Thr	His	Leu	Pro	Trp	Leu	Arg	
					125					130					135		
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	Glu	Arg	Leu	Leu	Ala	Ala	Gly	Gly	Thr	Val	Glu	Asp	Arg	Ala	Val	Thr	
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	Asp	Leu	Ala	Glu	Ala	Asp	Ala	Pro	Val	Val	Val	Asn	Cys	Thr	Gly	Leu	
			155					160					165				
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	Gln	Leu	Val	Val	Val	Glu	Asn	Pro	Gly	Ile	His	Asn	Trp	Leu	Val	Ala	
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	Arg	Leu	Leu	Leu	Gly	Gly	Thr	Ala	Glu	Glu	Asp	Ala	Trp	Ser	Thr	Glu	
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	Pro	Asp	Pro	Glu	Val	Ala	Ala	Ala	Ile	Val	Arg	Arg	Cys	Ala	Ala	Leu	
			235					240					245				
	cgt	ccc	gag	atc	gcc	gga	gcg	cgg	gtg	ctc	gcg	cac	ctg	gtg	ggg	ctg	822
	Arg	Pro	Glu	Ile	Ala	Gly	Ala	Arg	Val	Leu	Ala	His	Leu	Val	Gly	Leu	
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	Arg	Pro	Ala	Arg	Asp	Ala	Val	Arg	Leu	Glu	Arg	Gly	Thr	Leu	Pro	Asp	
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25	<p>Pro Ala Glu Arg Thr Thr Ser Val Val Ala Gly Gly Leu Trp Trp Pro</p> <p>35 40 45</p>			
	<p>Tyr Arg Ile Glu Pro Val Ala Leu Ala Gln Ala Trp Ala Leu Arg Ser</p> <p>50 55 60</p>			
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35	<p>Arg Met Leu Glu Gly Val Leu Gly Glu Thr Gly Leu Asp Glu Val Asp</p> <p>85 90 95</p>			
	<p>Gly Trp Ala Ala Ala Arg Leu Pro Gly Leu Arg Ala Ala Ser Ala Ala</p> <p>100 105 110</p>			
40	<p>Glu Tyr Ala Gly Thr Gly Leu Trp Ala Arg Leu Pro Leu Ile Asp Met</p> <p>115 120 125</p>			
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24

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26

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	Leu Gly Gly Val Lys Asp Glu Lys Val Tyr Pro Thr Arg Gly Gln Val	
	195 200 205	
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	Val Val Val Arg Ala Pro His Ile Gln Glu Asn Lys Met Arg Trp Gly	
	210 215 220	
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	Lys Asp Tyr Ala Thr Tyr Ile Ile Pro Arg Pro Tyr Ser Asn Gly Glu	
	225 230 235 240	
20	tta gtc tta ggt ggt ttc tta caa aag gat aat tgg aca ggt aat act	768
	Leu Val Leu Gly Gly Phe Leu Gln Lys Asp Asn Trp Thr Gly Asn Thr	
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25	ttt ggt ttt gaa act gat gat att gtt agt aga act aca tct tta tta	816
	Phe Gly Phe Glu Thr Asp Asp Ile Val Ser Arg Thr Thr Ser Leu Leu	
	260 265 270	
30	cca aag att tta gat gaa cca ctt cat att att aga gtt gca gct ggt	864
	Pro Lys Ile Leu Asp Glu Pro Leu His Ile Ile Arg Val Ala Ala Gly	
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	Leu Arg Pro Ser Arg His Gly Gly Pro Arg Ile Glu Ala Glu Val Cys	
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	Glu Glu Gly Lys Leu Thr Ile His Asn Tyr Gly Ala Ser Gly Tyr Gly	
	305 310 315 320	
45	tat caa gct ggt tat ggt atg tct tat gaa gct gtc aaa ctt tta gtt	1008
	Tyr Gln Ala Gly Tyr Gly Met Ser Tyr Glu Ala Val Lys Leu Leu Val	
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15

Ser Pro Trp Ala Gly Gly Asn Phe Ser Cys Ile Ser Pro Ala Asp Asp
 50 55 60

20 Thr Thr Leu Ala Tyr Asp Lys Phe Thr Tyr Leu Asn Leu Phe Lys Ile
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His Lys Lys Leu Gly Gly Pro Glu Cys Gly Leu Asp Asn Lys Pro Ser
 85 90 95

25 Thr Glu Tyr Trp Asp Phe Tyr Pro Gly Asp Glu Lys Val Asn Ser Leu
 100 105 110

Lys Gln Tyr Leu Lys Asp Phe Lys Val Ile Pro Lys Ser Glu Leu Pro
 115 120 125

30

Glu Gly Val Glu Tyr Gly Ile Ser Tyr Thr Thr Trp Asn Phe Asn Cys
 130 135 140

35 Pro Val Phe Leu Gln Asn Met Ala Asn Phe Leu Asn Lys Arg Asn Val
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Thr Ile Ile Arg Lys His Leu Thr His Ile Ser Gln Ala Tyr Leu Thr
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28

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<223> complementary: coding for pTOP10P tetracyclin regulatable promoter
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40 <223> complementary: coding for tetracyclin repressor rtTA
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45 <223> complementary: coding for Pisum sativum ptxA promoter

<220>

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